

SEQUENCE LISTENING



<110> Dahlqvist, Anders
 Stahl, Ulf
 Lenman, Marit
 Banas, Antoni
 Ronne, Hans
 Stymne, Sten

<120> PROCESSES FOR PRODUCING TRIACYLGLYCEROL USING GENES THAT ENCODE
 PHOSPHOLIPID:DIACYLGLYCEROL ACYLTRANSFERASES

<130> BASFnae337799PCT1-15

<140> US 09/937779

<150> PCT / EP 00 / 02701

<151> 2000-03-23

<160> 32

<170> PatentIn Ver. 3.3

<210> 1

<211> 1986

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> CDS

<222> (1)..(1983)

<400> 1

atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct	48
Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser	
1 5 10 15	
gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga	96
Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg	
20 25 30	
aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt	144
Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly	
35 40 45	
att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg	192
Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg	
50 55 60	
aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336

Gly	Ala	Tyr	His	Val	His	Asn	Ser	Asp	Ser	Asp	Leu	Phe	Asp	Asn	Phe	
			100					105					110			
gta	aat	ttt	gat	tca	ctt	aaa	gtg	tat	ttg	gat	gat	tgg	aaa	gat	gtt	384
Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val	
		115					120					125				
ctc	cca	caa	ggg	ata	agt	tcg	ttt	att	gat	gat	att	cag	gct	ggg	aac	432
Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn	
		130					135					140				
tac	tcc	aca	tct	tct	tta	gat	gat	ctc	agt	gaa	aat	ttt	gcc	ggt	ggt	480
Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Asp	Leu	Ser	Glu	Asn	Phe	Ala	Val	Gly	
145					150					155					160	
aaa	caa	ctc	tta	cgt	gat	tat	aat	atc	gag	gcc	aaa	cat	cct	ggt	gta	528
Lys	Gln	Leu	Leu	Arg	Asp	Tyr	Asn	Ile	Glu	Ala	Lys	His	Pro	Val	Val	
				165					170					175		
atg	gtt	cct	ggg	gtc	att	tct	acg	gga	att	gaa	agc	tgg	gga	gtt	att	576
Met	Val	Pro	Gly	Val	Ile	Ser	Thr	Gly	Ile	Glu	Ser	Trp	Gly	Val	Ile	
			180					185					190			
gga	gac	gat	gag	tgc	gat	agt	tct	gcg	cat	ttt	cgt	aaa	cgg	ctg	tgg	624
Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp	
			195				200					205				
gga	agt	ttt	tac	atg	ctg	aga	aca	atg	gtt	atg	gat	aaa	gtt	tgt	tgg	672
Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp	
	210					215					220					
ttg	aaa	cat	gta	atg	tta	gat	cct	gaa	aca	ggg	ctg	gac	cca	ccg	aac	720
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	
225					230					235					240	
ttt	acg	cta	cgt	gca	gca	cag	ggc	ttc	gaa	tca	act	gat	tat	ttc	atc	768
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	
				245					250					255		
gca	ggg	tat	tgg	att	tgg	aac	aaa	gtt	ttc	caa	aat	ctg	gga	gta	att	816
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	
			260				265					270				
ggc	tat	gaa	ccc	aat	aaa	atg	acg	agt	gct	gcg	tat	gat	tgg	agg	ctt	864
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	
		275					280					285				
gca	tat	tta	gat	cta	gaa	aga	cgc	gat	agg	tac	ttt	acg	aag	cta	aag	912
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys	
		290				295					300					
gaa	caa	atc	gaa	ctg	ttt	cat	caa	ttg	agt	ggg	gaa	aaa	gtt	tgt	tta	960
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu	
305					310					315					320	
att	gga	cat	tct	atg	ggg	tct	cag	att	atc	ttt	tac	ttt	atg	aaa	tgg	1008
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp	

325										330										335										
gtc	gag	gct	gaa	ggc	cct	ctt	tac	ggg	aat	ggg	ggg	cgt	ggc	tgg	gtt					1056										
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val															
			340					345					350																	
aac	gaa	cac	ata	gat	tca	ttc	att	aat	gca	gca	ggg	acg	ctt	ctg	ggc					1104										
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly															
		355					360					365																		
gct	cca	aag	gca	gtt	cca	gct	cta	att	agt	ggg	gaa	atg	aaa	gat	acc					1152										
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr															
	370					375					380																			
att	caa	tta	aat	acg	tta	gcc	atg	tat	ggg	ttg	gaa	aag	ttc	ttc	tca					1200										
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser															
385					390					395					400															
aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggg	ggg	ata	cca	tca					1248										
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser															
				405					410					415																
atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct					1296										
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser															
			420					425					430																	
tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att					1344										
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile															
		435					440					445																		
cga	ttt	gaa	agg	aat	acg	agc	gat	gct	ttc	aac	aaa	aat	ttg	aca	atg					1392										
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met															
	450					455					460																			
aaa	gac	gcc	att	aac	atg	aca	tta	tcg	ata	tca	cct	gaa	tgg	ctc	caa					1440										
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln															
465					470					475					480															
aga	aga	gta	cat	gag	cag	tac	tcg	ttc	ggc	tat	tcc	aag	aat	gaa	gaa					1488										
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu															
				485					490					495																
gag	tta	aga	aaa	aat	gag	cta	cac	cac	aag	cac	tgg	tcg	aat	cca	atg					1536										
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met															
			500					505					510																	
gaa	gta	cca	ctt	cca	gaa	gct	ccc	cac	atg	aaa	atc	tat	tgt	ata	tac					1584										
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr															
		515					520					525																		
ggg	gtg	aac	aac	cca	act	gaa	agg	gca	tat	gta	tat	aag	gaa	gag	gat					1632										
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp															
	530					535					540																			
gac	tcc	tct	gct	ctg	aat	ttg	acc	atc	gac	tac	gaa	agc	aag	caa	cct					1680										
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro															
545					550					555					560															

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 2

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 2

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val	115	120	125
Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn	130	135	140
Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Asp	Leu	Ser	Glu	Asn	Phe	Ala	Val	Gly	145	150	155
Lys	Gln	Leu	Leu	Arg	Asp	Tyr	Asn	Ile	Glu	Ala	Lys	His	Pro	Val	Val	165	170	175
Met	Val	Pro	Gly	Val	Ile	Ser	Thr	Gly	Ile	Glu	Ser	Trp	Gly	Val	Ile	180	185	190
Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp	195	200	205
Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp	210	215	220
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn	225	230	235
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile	245	250	255
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile	260	265	270
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu	275	280	285
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys	290	295	300
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu	305	310	315
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp	325	330	335
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val	340	345	350
Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly	355	360	365
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	370	375	380
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	385	390	395
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	405	410	415

Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 3

<211> 2312

<212> genomic DNA

<213> Schizosaccharomyces pombe

<400> 3

atggcgtcctt ccaagaagag caaaactcat aagaaaaaga aagaagtcaa atctcctatc 60
 gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgtccgaa 120

```

acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
ttgggcgcta ttttgggaat atgcggtgct ttttttttcg ctgttggaga cgacaatgct 240
gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttggtt 300
gatgacatta aaggatattt atcttataat gtgtttaagg atgcaccttt tactacggac 360
aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tgttattatg gttcctgggtg ttatcagctc aggattagaa 480
agttggtcgt ttaataattg ctcgattcct tacttttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatgtt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaccg gcttggatcc gaagggaatt aagctgcgag cagctcaggg gtttgaagca 660
gctgattttt ttatcacggg ctattggatt tggagtaaa taattgaaaa ccttgctgca 720
attggttatg agcctaataa catgttaagt gcttcttacg attggcgggt atcatatgca 780
aatttagagg aacgtgataa atatttttca aagttaaaaa tggtcattga gtacagcaac 840
attgtacata agaaaaaggt agtgttgatt tctcactcca tgggttcaca gggtacgtac 900
tattttttta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaat 960
gatcatattg aagcatttat aaatgtgagt ctcgatggtt gtttgactac gtttctaact 1020
tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
ggtgaaatga aagatacagg tattgtaatt acattaaaca tgtaaatatt taatttttgc 1140
taaccgtttt aagctcaatt gaatcagttt tccggtctatg ggtaagcaat aaattgttga 1200
gatttgttac taatttactg tttagtttgg aaaaattttt tcccgttct gaggtatatt 1260
caaaaataca aatgtgctct actttttcta acttttaata gagagccatg atggttcgca 1320
ctatgggagg agttagttct atgcttccta aaggaggcga tgttgatagg ggaaatgcca 1380
gttgggtaag aaatatgtgc tgtaattttt ttattaatat ttaggctcca gatgatctta 1440
atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
acgatgaatt tgacatagat gatgcattac aattttttaa aaatgttaca gatgacgatt 1560
ttaaagtcac gctagcgaat aattattccc acggtcttgc ttggactgaa aaagaagtgt 1620
taaaaaataa cgaaatgccg tctaaatgga taaatccgct agaagtaaga acattaaagt 1680
tactaaatta tactaaccca aatagactag tcttccttat gctcctgata tgaaaattta 1740
ttgcgttcac ggggtcggaa aaccaactga gagaggttat tattatacta ataatcctga 1800
ggggcaacct gtcattgatt cctcgggtta tgatggaaca aaagttgaaa atgtgagaga 1860
atttatgttt caaacattct attaaactgtt ttattagggg attgttatgg atgatgggta 1920
tggaacttta ccaatattag cccttggttt ggtgtgcaat aaagtttggc aaacaaaaag 1980
gtttaatcct gctaatacaa gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
tgatctgaga ggaggacctc gctcggcaga acacgtcgat atacttgac attcagagct 2100
aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
ttttaaaagt ttcacacagg catggtgact cggtaacaaa ccgttatata tcagatatcc 2220
agtacggaca taagttttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
atgagataaa tctcgataaa cctagaaatt aa 2312

```

<210> 4

<211> 3685

<212> genomic DNA

<213> Arabidopsis thaliana

<400> 4

```

atgcccctta ttcacgcgaa aaagccgacg gagaaaccat cgacgccgcc atctgaagag 60
gtggtgcacg atgaggattc gcaaaagaaa ccacacgaat cttccaaatc ccaccataag 120
aaatcgaacg gaggaggaa gtggtcgtgc atcgattctt gttgttggtt cattgggtgt 180
gtgtgtgtaa cctgggtggt tcttctcttc tttacaacg caatgcctgc gagcttcct 240
cagtatgtaa cggagcgaat cacgggtcct ttgcctgacc cgccgggtgt taagctcaaa 300
aaagaaggtc ttaaggcgaa acatcctgtt gtcttcattc ctgggattgt caccgggtgg 360
ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaaacg tttgtgggg 420
ggaaactttt gtgaagtcta caaaagggtg gctcaacaat tctcactctt cctttatatt 480
gggatttgga ttggatctga tgagatcacg cacttggtgc ttcttcaaca tcaactcaaa 540
tttaattcca tgtttgtctg tcttactctt tactttttt tttttttgat gtgaaacgct 600
attttcttaa gagactattt ctgtatgtgt aaggtaaagc ttccaaggac gtaattggct 660
tggtactatt ctgtttgatt gttaacttta ggatataaaa tagctgcctt ggaatttcaa 720

```

```

gtcatcttat tgccaaatct gttgctagac atgccctaga gtccgttcat aacaagttac 780
ttcctttact gtcgttgcgt gtagatttag ctttgtgtag cgtataatga agtagtgttt 840
tatgttttgt tgggaataga gaagttctaa ctacatctgt ggaaagtgtg ttcaggctgt 900
gatagaggac tgttgcttta ttattcaact atgtatatgt gtaattaaag ctagtccctt 960
tttgatcttt cagctcaatg tgcttttctc aatttttttc tcaatttcaa agtttcacat 1020
cgagtttatt cacatgtctt gaatttcgtc catcctcggt ctgttatcca gctttgaact 1080
cctcccgacc ctgctatgga tatattaaaa aaaaagtgtt ttgtgggttg catctttgtt 1140
acgatctgca tcttcttctt tcggctcagt gttcatgttt ttgctatggt agagatgggc 1200
aatgttattg ttgatggtaa cagtgggata gttgatagta tcttaactaa tcaattatct 1260
ctttgattca ggcctctatg ttgggtggaa cacatgtcac ttgacaatga aactgggttg 1320
gatccagctg gtattagagt tcgagctgta tcaggactcg tggctgctga ctactttgtc 1380
cctggctact ttgtctgggc agtgcgtatt gctaaccctg cacatatggg atatgaagag 1440
aaaaatatgt acatggctgc atatgactgg cggctttcgt ttcagaacac agaggttctt 1500
ttctcatcgt tctttctatt attctgttcc atgttacgtt tctttcttca ttacttaagg 1560
cttaaatatg tttcatgttg aattaatagg tacgtgatca gactcttagc cgtatgaaaa 1620
gtaatataga gttgatgggt tctaccaacg gtggaaaaaa agcagttata gttccgcatt 1680
ccatgggggt cttgtatttt ctacatttta tgaagtgggt tgaggcacca gtcctctgtg 1740
gtggcggggg tgggccagat tgggtgtgca agtatattaa ggcggtgatg aacattgggtg 1800
gaccatttct tgggtgtcca aaagctgttg cagggtcttt ctctgctgaa gcaaaggatg 1860
ttgcagttgc caggtattga atatctgctt atacttttga tgatcagaac cttggctctg 1920
gaactcaaag ttattctact aaatatcaat tctaataaca ttgctatatt atcgctgcaa 1980
ctgacattgg ttgattattt ttgctgctta tgtaactgaa actctcttga gattagacaa 2040
atgatgaatt gataattctt acgcattgct ctgtgatgac cagtttctta gcttcgacga 2100
taacatttgt catactgtct tttggagggc attgaatttt gctatggaaa gcgctggagc 2160
ttccatgctt gcattcttta ccaattagcg ttattctgct tctttcaatt ttcttgata 2220
tgcatctatg gtcttttatt tcttcttaat taaagactcg ttggattagt tgctctatta 2280
gtcacttgggt tccttaatat agaactttac tttcttcgaa aattgcagag cgattgcccc 2340
aggattctta gacaccgata tatttagact tcagacctg cagcatgtaa tgagaatgac 2400
acgcacatgg gactcaacaa tgtctatgtt accgaaggga ggtgacacga tatggggcgg 2460
gcttgattgg tcaccggaga aaggccacac ctgtgtgggg aaaaagcaaa agaacaacga 2520
aacttgtggg aaagcagggtg aaaacggagt ttccaagaaa agtcctgtta actatggaag 2580
gatgatattc tttgggaaag aagtagcaga ggctgcgcca tctgagatta ataatttga 2640
ttttcgagta aggacatata aatcataata aaccttgtac attttgtgat tgtatgatga 2700
atatctgtac attttatctg gtgaagggtg ctgtcaaagg tcagagtatc ccaaatacaca 2760
cctgtcgtga cgtgtggaca gaggaccatg acatgggaat tgctgggatc aaagctatcg 2820
ctgagtataa ggtctacact gctggtgaag ctatagatct actacattat gttgctccta 2880
agatgatggc gcgtgggtgcc gctcatttct cttatggaaat tgctgatgat ttggatgaca 2940
ccaagtatca agatcccaaa tactgggtcaa atccgttaga gacaaagtaa gtgatttctt 3000
gattccaact gtatccttcg tcctgatgca ttatcagctt ttttgttttc ggtcttgttg 3060
gatatggttt tcagctcaaa gcttacaaaag ctgtttctga gcctttctca aaaaggcttg 3120
ctcagtaata ttgaggtgct aaagttgata catgtgactc ttgcttataa atcctccgtt 3180
tggtttgttc tgctttttca gattaccgaa tgctcctgag atggaaatct actcattata 3240
cggagtgggg ataccaacgg aacgagcata cgtatacaag cttaccaggt ctcccgacag 3300
ttgcatcccc tttcagatat tcacttctgc tcacgaggag gacgaagata gctgtctgaa 3360
agcaggagtt tacaatgtgg atggggatga aacagtaccc gtctaagtg ccgggtacat 3420
gtgtgcaaaa gcgtggcgtg gcaagacaag attcaaccct tccggaatca agacttatat 3480
aagagaatac aatcactctc cgccggctaa cctgttgga gggcgcgga cgagagtgg 3540
tgcccatggt gatatcatgg gaaactttgc tttgatcgaa gatatcatga ggggtgccc 3600
cggaggtaac gggctctgata taggacatga ccaggtccac tctggcatat ttgaatggtc 3660
ggagcgtatt gacctgaagc tgtga 3685

```

<210> 5

<211> 2427

<212> cDNA

<213> Arabidopsis thaliana

<400> 5

```

agaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60
ctggacgaga tttgacaaaag tccgtatagc ttaacctggg ttaatttcaa gtgacagata 120
tgcccccttat tcatcggaag aagccgacgg agaaaccatc gacgccgcca tctgaagagg 180
tggtgcacga tgaggattcg caaaagaaac cacacgaatc ttccaaatcc caccataaga 240
aatcgaacgg aggaggggaag tggctgtgca tcgattcttg ttgttgggtc attgggtgtg 300
tgtgtgtaac ctggtggttt cttctcttcc tttacaacgc aatgcctgcg agcttccctc 360
agtatgtaac ggagcgaatc acgggtcctt tgectgaccc gcccggtgtt aagctcaaaa 420
aaagaaggtc ttaaggcgaa acatcctggt gtcttcattc ctgggattgt caccggtggg 480
ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaaacg tttgtggggg 540
ggaacttttg gtgaagtcta caaaaggcct ctatggtggg tggaacacat gtcacttgac 600
aatgaaaactg ggttgatcc agctggtatt agagttcgag ctgtatcagg actcgtggct 660
gtgactact ttgctcctgg ctactttgtc tgggcagtgc tgattgctaa ccttgcacat 720
attggatatg aagagaaaaa tatgtacatg gctgcatatg actggcggct ttcgtttcag 780
aacacagagg tacgtgatca gactcttagc cgtatgaaaa gtaatataga gttgatgggt 840
tctaccaacg gtggaaaaaa agcagttata gttccgcatt ccatgggggt cttgtatttt 900
ctacatttta tgaagtgggt tgaggcacca gtcctctggt gtggcggggg tgggccagat 960
tggtgtgcaa agtatattaa ggcggtgatg aacattgggtg gaccatttct tgggtgtcca 1020
aaagctgttg cagggtcttt ctctgctgaa gcaaaggatg ttgcagttgc cagagcgatt 1080
gccccaggat tcttagacac cgatatatct agacttcaga ccttgcagca tgtaatgaga 1140
atgacacgca catgggactc aacaatgtct atgttaccga agggagggtg cacgatatgg 1200
ggcgggcttg attggtcacc ggagaaaggc cacacctgtt gtgggaaaaa gcaaaagaac 1260
aacgaaactt gtggtgaagc aggtgaaaac ggagtttcca agaaaagtcc tgttaactat 1320
ggaaggatga tatcttttgg gaaagaagta gcagaggctg cgccatctga gattaataat 1380
attgattttc gaggtgctgt caaaggctcag agtatcccaa atcacacctg tctgacgtg 1440
tggaacagag accatgacat gggaattgct gggatcaaag ctatcgctga gtataaggct 1500
tacctgctg gtgaagctat agatctacta cattatgttg ctctaagat gatggcgcgt 1560
ggtgccgctc atttctctta tggaattgct gatgatttg atgacaccaa gtatcaagat 1620
cccaaactg ggtcaaatcc gttagagaca aaattaccga atgctcctga gatggaaatc 1680
tactcattat acggagtggg gataccaacg gaacgagcat acgtatacaa gcttaaccag 1740
tctcccgaca gttgcacccc ctttcagata ttcacttctg ctcacgagga ggacgaagat 1800
agctgtctga aagcaggagt ttacaatgtg gatggggatg aaacagtacc cgtcctaagt 1860
gccgggtaca tgtgtgcaaa agcgtggcgt ggcaagacaa gattcaacct ttccggaatc 1920
aagacttata taagagaata caatcactct ccgccggcta acctgttgga agggcgcggg 1980
acgcagagtg gtgcccatgt tgatatcatg ggaaactttg ctttgatcga agatatcatg 2040
agggttgccg ccggaggtaa cgggtctgat ataggacatg accagggtcca ctctggcata 2100
tttgaatggt cggagcgtat tgacctgaag ctgtgaatat catgatctct ttaagctgtc 2160
ctgtcagctt atgtgaatcc aatactttga aagagagatc atcatcaatt catcatcatc 2220
gtcatcatca tgatgctcaa ctacaaaaga agcctgagaa tgatactttg gtgcgaaatt 2280
ctcaatacct ctttaatat cttattgaat gtaaattata caatcctatc taatgtttga 2340
acgataacac aaaacttgct gcngccatgt ttgtttgtct tgtcaaaagc atcaatttgt 2400
gggttaaaaa aaaaaaaaaa aaaaaaa 2427

```

<210> 6

<211> 671

<212> PRT

<213> *Arabidopsis thaliana*

<400> 6

```

Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
  1                      5                      10                     15

```

```

Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
      20                      25                     30

```

```

Glu Ser Ser Lys Ser His His Lys Lys Ser Asn Gly Gly Gly Lys Trp

```


His Val Met Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu
 340 345 350
 Pro Lys Gly Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu
 355 360 365
 Lys Gly His Thr Cys Cys Gly Lys Lys Gln Lys Asn Asn Glu Thr Cys
 370 375 380
 Gly Glu Ala Gly Glu Asn Gly Val Ser Lys Lys Ser Pro Val Asn Tyr
 385 390 395 400
 Gly Arg Met Ile Ser Phe Gly Lys Glu Val Ala Glu Ala Ala Pro Ser
 405 410 415
 Glu Ile Asn Asn Ile Asp Phe Arg Gly Ala Val Lys Gly Gln Ser Ile
 420 425 430
 Pro Asn His Thr Cys Arg Asp Val Trp Thr Glu Tyr His Asp Met Gly
 435 440 445
 Ile Ala Gly Ile Lys Ala Ile Ala Glu Tyr Lys Val Tyr Thr Ala Gly
 450 455 460
 Glu Ala Ile Asp Leu Leu His Tyr Val Ala Pro Lys Met Met Ala Arg
 465 470 475 480
 Gly Ala Ala His Phe Ser Tyr Gly Ile Ala Asp Asp Leu Asp Asp Thr
 485 490 495
 Lys Tyr Gln Asp Pro Lys Tyr Trp Ser Asn Pro Leu Glu Thr Lys Leu
 500 505 510
 Pro Asn Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile
 515 520 525
 Pro Thr Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser
 530 535 540
 Cys Ile Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp
 545 550 555 560
 Ser Cys Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val
 565 570 575
 Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys
 580 585 590
 Thr Arg Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn
 595 600 605
 His Ser Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly
 610 615 620
 Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met
 625 630 635 640

Arg Val Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val
645 650 655

His Ser Gly Ile Phe Glu Trp Ser Glu Arg Ile Asp Leu Lys Leu
660 665 670

<210> 7
 <211> 643
 <212> cDNA
 <213> Zea mays

<220>
 <221> CDS
 <222> (1)..(402)

<400> 7
 cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15
 gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30
 tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45
 aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95
 ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110
 ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
 Leu Lys Leu
 115
 gcg ttc caa agt gtc ctg cctgagtgcactctggatt ttgcttaaat 432
 attgtaattt ttcacgcttc attcgctcct ttgtcaaatt tacatttgac aggacgccaa 492
 tgcgatacga tggtgtaccg ctattttcag cattgtatat taaactgtac aggtgtaagt 552
 tgcatttgcc agctgaaatt gtgtagtcgt tttctttacg atttaatancc aagtggcgga 612
 gcagtgcccc aagcnaaaaa aaaaaaaaaa a 643

<210> 8
 <211> 115
 <212> PRT
 <213> Zea mays

<400> 8
 Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
 1 5 10 15
 Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
 20 25 30
 Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
 35 40 45
 Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
 50 55 60
 Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
 65 70 75 80
 Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
 85 90 95
 Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
 100 105 110
 Leu Lys Leu
 115

<210> 9
 <211> 616
 <212> cDNA
 <213> Neurospora crassa

<400> 9
 ggtggcgaag acganggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
 accctctaga gacacgacta ccnttgcacc cagcctcaag gtntacngtt tntatgggta 120
 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcac 180
 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggg gtgattttgg 240
 gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
 cagaacgggt caatccgaga ggagggccga atacggcgga tcacgtggat attctaggaa 420
 ggacgaatct aaacgagtac attcttaaag tggcggcagg tcgaggcgat acaattgagg 480
 attttattac tagtaattatt cttaaataatg tagaaaagggt tgaaatttat gaagagtaat 540
 taaatacggc acatagggtta ctcaatagta tgactaatta aaaaaaaatt ttttttctaa 600
 aaaaaaaaaa aaaaaa 616

<210> 10
 <211> 1562
 <212> genomic DNA
 <213> Arabidopsis thaliana

<400> 10
 atgaaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcgttgt ggtgacgatg 60
 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattctgggt tccaggaaac 120
 ggaggttaacc agctagaggt acggctggac agagaataca agccaagtag tgtctgggtgt 180
 agcagctgggt tatatccgat tcataagaag agtgggtggat ggtttaggct atgggttcgat 240
 gcagcagtgt tattgtctcc cttcaccagg tgcttcagcg atcgaatgat gttgtactat 300
 gaccctgatt tggatgatta ccaaaatgct cctggtgtcc aaaccgggt tcctcatttc 360
 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggtagtagtact ttccaagata 420
 tatcatttttg ggacatttgc ataatagaaca aaatagacat aaatttgggg gattattgtt 480

atatcaatat	ccattttatat	gctagtcggt	aatgtgagtg	ttatgttagt	atagttaatg	540
tgagtgttat	gtgattttcc	atttttaaatg	aagctagaaa	gttgctcgtt	aataatgttg	600
ctatgtcatg	agaattataa	ggacactatg	taaatgtagc	ttaataataa	ggtttgattt	660
gcagagatgc	cacatcttac	atggaacatt	tggtgaaaagc	tctagagaaa	aaatgcgggt	720
atgttaacga	ccaaaccatc	ctaggagctc	catatgattt	caggtagcgc	ctggctgctt	780
cgggccaccc	gtcccgtgta	gcctcacagt	tcctacaaga	cctcaaacia	ttgggtggaaa	840
aaactagcag	cgagaacgaa	ggaaagccag	tgatactcct	ctcccatagc	ctaggaggac	900
ttttcgtcct	ccatttcctc	aaccgtacca	ccccttcattg	gcgccgcaag	tacatcaaac	960
actttgttgc	actcgctgcg	ccatgggggtg	ggacgatctc	tcagatgaag	acatttgctt	1020
ctggcaacac	actcggtgtc	ccttttagtta	accctttgct	ggtcagacgc	catcagagga	1080
cctccgagag	taaccaatgg	ctacttccat	ctaccaaagt	gtttcacgac	agaactaaac	1140
cgcttgctgt	aactccccag	gttaactaca	cagcttacga	gatggatcgc	ttttttgcag	1200
acattggatt	ctcacaagga	gttgtgcctt	acaagacaag	agtgttgctt	ttaacagagg	1260
agctgatgac	tccgggagtg	ccagtcactt	gcataatgg	gagaggagtt	gatacaccgc	1320
aggttttgat	gtatggaaaa	ggaggattcg	ataagcaacc	agagattaag	tatggagatg	1380
gagatgggac	ggtaattttg	gcgagcttag	cagctttgaa	agtcgatagc	ttgaacaccg	1440
tagagattga	tggagtttcg	catacatcta	tacttaaaga	cgagatcgca	cttaaagaga	1500
ttatgaagca	gattttcaatt	attaattatg	aattagccaa	tgtaaatgcc	gtcaatgaat	1560
ga						1562

<210> 11

<211> 3896

<212> genomic DNA

<213> Arabidopsis thaliana

<400> 11

atgggagcga	attcgaaatc	agtaacggct	tccttcaccg	tcacgcgcgt	ttttttcttg	60
atttgccgtg	gccgaactgc	ggtggaggat	gagaccgagt	ttcacggcga	ctactcgaag	120
ctatcgggta	taatcattcc	gggatttgcg	tcgacgcagc	tacgagcgtg	gtcgatcctt	180
gactgtccat	acactccggt	ggacttcaat	ccgctcgacc	tcgtatggct	agacaccact	240
aagggtccgtg	atcttcattt	ccttcgctcc	ttattctgtc	ggtcgagtca	cttggttgatg	300
aattccaagc	gaaatatagc	aatgaagcat	gtctcgtctc	tccttattgat	tcgttcatta	360
gtcaacagtg	acgcttctga	atctgagttt	agagtcatat	aaaacagctg	actcggcgag	420
tgtttcccat	cgcttttggt	tcgctaaatg	tagcgcaatg	aatgtgtaat	tagtctgcgc	480
tttttattca	actagatctg	caagtttttc	agagtgtctc	atagtagtta	gaaaatgtta	540
ggtcatttta	cttggtgcatt	gtgattcttt	tgggtgttgc	ttactgatcg	acgtgatgga	600
tggtttacag	cttctttctg	ctgtcaactg	ctggtttaag	tgtatgggtc	tagatcctta	660
taatcaaaca	gaccatcccg	agtgtaaagc	acggcctgac	agtggctctt	cagccatcac	720
agaattggat	ccaggttaca	taacaggtag	tttcggattt	ttctttcttt	tgagttttct	780
tcaatttgat	atcatcttgt	tgtgatataa	tatggctaag	ttcattaatt	tgggtcaattt	840
tcaggtcctc	tttctactgt	ctggaaagag	tggcttaagt	ggtgtgttga	gttttggtata	900
gaagcaaagt	caattgtcgc	tgttccatac	gattggagat	tgtcaccaac	caaattggaa	960
gagcgtgacc	tttactttca	caagctcaag	ttagtccctta	tcaggctaat	gtctttttatc	1020
ttctcttttt	atgtaagata	agctaagagc	tctggctcgtc	ttcctttttg	caggttgacc	1080
tttgaaactg	ctttaaaact	ccgtggcggc	ccttctatag	tatttgccca	ttcaatgggt	1140
aataatgtct	tcagatactt	tctggaatgg	ctgaggctag	aaattgcacc	aaaacattat	1200
ttgaagtggc	ttgatcagca	tatccatgct	tatttcgctg	ttggtagcgc	cctactatcc	1260
ttaaagtacc	attttatttt	ttctctaatt	gggggagtta	tgttgtagct	tgttgagattg	1320
agctcgatac	ctgatttggt	gttgatttag	gagctcctct	tccttggtct	gttgaggcaa	1380
tcaaactctac	tctctctggg	gtaacgtttg	gccttcctgt	ttctgagggt	acctctgact	1440
tctcttttagt	tttaagtagt	tgatatcaac	caggctctat	aactcactgg	attttccttt	1500
tgaagtattt	acttttggtt	attgaactgc	tgtacgcgat	atggtagctg	tagatcttga	1560
agtgttagtt	atcaaagaac	atattgtggg	tagtatacct	gtcagcggcc	ttagctaata	1620
caaccaaac	acatgtacac	tgatttagtt	ttcagattat	tatggtagac	tttaagttga	1680
gaagaaactt	tgactgaaat	ctttttattt	taataggcta	tgatttggtt	attgaaatca	1740
tgtgacatat	tgacatgcgc	ttctcatggt	ttttgttggc	aaggcttcag	ggaactgctc	1800

```

ggttgttgct caattctttt gcgtcgctcat tgtggccttat gccatttttca aagaattgca 1860
agggtgataa cacattctgg acgcattttt ctgggggtgc tgcaaagaaa gataagcgcg 1920
tataccactg tgatgaagag gaatatcaat caaaatattc tggctggccg acaaattatta 1980
ttaacattga aattccttcc actagcggtt agactctgta tatgcaactg taacactaac 2040
aaaagtttca ccaagaatgt tcactctcat atttcgttcc tttgatgtgt atccatcagt 2100
tacagaaaac gctctagtca acatgaccag catggaatgt ggccctccca cctttttgtc 2160
tttcacagcc cgtgaactag cagatgggac tcttttcaaa gcaatagaag actatgaccc 2220
agatagcaag aggatgttac accagttaaa gaagtacgta cctttctttg tgataagaaa 2280
tattgctcat cgatcatcac ttgctggcct cttgtacgta aaattgtttt gtttaaatct 2340
ctatatcaat tgttcatatg ctttgccttt cttactataa gaaacaagta taatcagaaa 2400
ccttattatt gattatcagt tctctcctta tattatggaa tgtctttttc gtttacagtt 2460
atgaatgcaa aagggggtat tttagttgat tgattctctc attctctagt ttgttttgac 2520
taatagcgct aattttgttt ttctagcaaa tctttgtgaa ttatatataa catgctaact 2580
atacttttca ggttgtatca tgatgacctt gtttttaatc ctctgactcc ttgggagaga 2640
ccacctataa aaaatgtatt ttgcatatat ggtgctcatc taaagacaga ggtatgatgc 2700
attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgcaata 2760
tctttttgaa ttatgattta tcttctccct tgcactctat gctattaagc gttaaaggta 2820
ctaaatgtat gaagctgtct gtcatagggt gggtattact ttgccccaa gggcaaacct 2880
tatcctgata attggatcat cacggatatt atttatgaaa ctgaagggtc cctcgtgtca 2940
aggtaathtt ccgcaatggc agaagtaaaa caggaaggca aagtccttctg tatcagtcta 3000
gtggcatggt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
ttatcattcc ttttgagctt agtggatgat cagtggctta aagtgggaag aggtgttgca 3120
tgaaacatga cacttgatc aaagataact agcaaaacaa aactaaccct tttctgaatt 3180
tcatattatt aggagtagtc gtgcttttaa aaaatttggt ttaagaaacc gaaaaactag 3240
ttcatatcct gattgtgcaa tatctgcagg tctggaactg tggttgatgg gaacgctgga 3300
cctataactg gggatgagac ggtaagctca gaagtgggtt ttgaaattat cttcttgcaa 3360
actactgaag actaagataa tacttgcttc tggaaactg cttgctatgt tctctagtac 3420
actgcaatat tgactctccg ctacttttat tgattatgaa attgatctct tataggtacc 3480
ctatcattca ctctcttggt gcaagaattg gctcggacct aaagttaaca taacaatggc 3540
tccccaggta ctctttttta gttcctcacc ttatatagat caaactttta gtgtactttt 3600
ctggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
cctcaagaac ttgtattaat ctaaacgaga ttctcattgg gaaaataaaa caacagccag 3720
aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggtcagaca 3780
tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840
agagcattcc ggggaagaga accgcagctc gggagcttga taaaagtggg tattaa 3896

```

<210> 12

<211> 709

<212> cDNA

<213> *Lycopersicon esculentum*

<400> 12

```

ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
aagtgcattc aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120
tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgcagatct ccagctttga 240
tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
ttacaaaagg ttgtgtctga tcctcactat tttcttctat aaatgtttga gtttgtattg 360
acattgtaag tattgcaaca aaaagcaaa gctgggcctc tgagggatga ggactgctat 420
tggtgattac ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480
tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacct tccccggtca 540
caacgatgca gatatgtatt cggggatgtt cacctgggac agagttgcag attgaagagt 600
tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaac 660
aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709

```

<210> 13
 <211> 623
 <212> PRT
 <213> Schizosaccharomyces pombe

<400> 13

Met	Ala	Ser	Ser	Lys	Lys	Ser	Lys	Thr	His	Lys	Lys	Lys	Lys	Glu	Val
1				5					10					15	
Lys	Ser	Pro	Ile	Asp	Leu	Pro	Asn	Ser	Lys	Lys	Pro	Thr	Arg	Ala	Leu
			20					25					30		
Ser	Glu	Gln	Pro	Ser	Ala	Ser	Glu	Thr	Gln	Ser	Val	Ser	Asn	Lys	Ser
		35					40					45			
Arg	Lys	Ser	Lys	Phe	Gly	Lys	Arg	Leu	Asn	Phe	Ile	Leu	Gly	Ala	Ile
	50					55					60				
Leu	Gly	Ile	Cys	Gly	Ala	Phe	Phe	Phe	Ala	Val	Gly	Asp	Asp	Asn	Ala
65					70					75					80
Val	Phe	Asp	Pro	Ala	Thr	Leu	Asp	Lys	Phe	Gly	Asn	Met	Leu	Gly	Ser
				85					90				95		
Ser	Asp	Leu	Phe	Asp	Asp	Ile	Lys	Gly	Tyr	Leu	Ser	Tyr	Asn	Val	Phe
			100					105					110		
Lys	Asp	Ala	Pro	Phe	Thr	Thr	Asp	Lys	Pro	Ser	Gln	Ser	Pro	Ser	Gly
		115					120					125			
Asn	Glu	Val	Gln	Val	Gly	Leu	Asp	Met	Tyr	Asn	Glu	Gly	Tyr	Arg	Ser
	130					135					140				
Asp	His	Pro	Val	Ile	Met	Val	Pro	Gly	Val	Ile	Ser	Ser	Gly	Leu	Glu
145					150					155					160
Ser	Trp	Ser	Phe	Asn	Asn	Cys	Ser	Ile	Pro	Tyr	Phe	Arg	Lys	Arg	Leu
				165					170					175	
Trp	Gly	Ser	Trp	Ser	Met	Leu	Lys	Ala	Met	Phe	Leu	Asp	Lys	Gln	Cys
			180					185					190		
Trp	Leu	Glu	His	Leu	Met	Leu	Asp	Lys	Lys	Thr	Gly	Leu	Asp	Pro	Lys
		195				200						205			
Gly	Ile	Lys	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ala	Ala	Asp	Phe	Phe
	210					215					220				
Ile	Thr	Gly	Tyr	Trp	Ile	Trp	Ser	Lys	Val	Ile	Glu	Asn	Leu	Ala	Ala
225					230					235					240
Ile	Gly	Tyr	Glu	Pro	Asn	Asn	Met	Leu	Ser	Ala	Ser	Tyr	Asp	Trp	Arg
				245				250						255	

Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
 260 265 270
 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
 275 280 285
 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
 290 295 300
 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
 305 310 315 320
 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
 325 330 335
 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
 340 345 350
 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
 355 360 365
 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
 370 375 380
 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
 385 390 395 400
 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
 405 410 415
 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
 420 425 430
 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala
 435 440 445
 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
 450 455 460
 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
 465 470 475 480
 Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
 485 490 495
 Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
 500 505 510
 Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
 515 520 525
 Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
 530 535 540
 Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
 545 550 555 560

His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
565 570 575

His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
580 585 590

Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
595 600 605

Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
610 615 620

<210> 14

<211> 432

<212> PRT

<213> *Arabidopsis thaliana*

<400> 14

Met Lys Lys Ile Ser Ser His Tyr Ser Val Val Ile Ala Ile Leu Val
1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
 210 215 220
 Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro
 225 230 235 240
 Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
 245 250 255
 Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
 260 265 270
 Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
 275 280 285
 Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
 290 295 300
 Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
 305 310 315 320
 Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
 325 330 335
 Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
 340 345 350
 Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
 355 360 365
 Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
 370 375 380
 Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
 385 390 395 400
 Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
 405 410 415
 Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
 420 425 430

<210> 15

<211> 552

<212> PRT

<213> Arabidopsis thaliana

<400> 15

Met Gly Ala Asn Ser Lys Ser Val Thr Ala Ser Phe Thr Val Ile Ala
 1 5 10 15
 Val Phe Phe Leu Ile Cys Gly Gly Arg Thr Ala Val Glu Asp Glu Thr
 20 25 30

Glu	Phe	His	Gly	Asp	Tyr	Ser	Lys	Leu	Ser	Gly	Ile	Ile	Ile	Pro	Gly
		35					40					45			
Phe	Ala	Ser	Thr	Gln	Leu	Arg	Ala	Trp	Ser	Ile	Leu	Asp	Cys	Pro	Tyr
	50					55					60				
Thr	Pro	Leu	Asp	Phe	Asn	Pro	Leu	Asp	Leu	Val	Trp	Leu	Asp	Thr	Thr
	65				70					75					80
Lys	Leu	Leu	Ser	Ala	Val	Asn	Cys	Trp	Phe	Lys	Cys	Met	Val	Leu	Asp
				85					90					95	
Pro	Tyr	Asn	Gln	Thr	Asp	His	Pro	Glu	Cys	Lys	Ser	Arg	Pro	Asp	Ser
			100					105					110		
Gly	Leu	Ser	Ala	Ile	Thr	Glu	Leu	Asp	Pro	Gly	Tyr	Ile	Thr	Gly	Pro
		115					120					125			
Leu	Ser	Thr	Val	Trp	Lys	Glu	Trp	Leu	Lys	Trp	Cys	Val	Glu	Phe	Gly
	130					135					140				
Ile	Glu	Ala	Asn	Ala	Ile	Val	Ala	Val	Pro	Tyr	Asp	Trp	Arg	Leu	Ser
145					150					155					160
Pro	Thr	Lys	Leu	Glu	Glu	Arg	Asp	Leu	Tyr	Phe	His	Lys	Leu	Lys	Leu
				165					170					175	
Thr	Phe	Glu	Thr	Ala	Leu	Lys	Leu	Arg	Gly	Gly	Pro	Ser	Ile	Val	Phe
			180					185					190		
Ala	His	Ser	Met	Gly	Asn	Asn	Val	Phe	Arg	Tyr	Phe	Leu	Glu	Trp	Leu
		195					200					205			
Arg	Leu	Glu	Ile	Ala	Pro	Lys	His	Tyr	Leu	Lys	Trp	Leu	Asp	Gln	His
	210					215					220				
Ile	His	Ala	Tyr	Phe	Ala	Val	Gly	Ala	Pro	Leu	Leu	Gly	Ser	Val	Glu
225					230					235					240
Ala	Ile	Lys	Ser	Thr	Leu	Ser	Gly	Val	Thr	Phe	Gly	Leu	Pro	Val	Ser
				245					250					255	
Glu	Gly	Thr	Ala	Arg	Leu	Leu	Ser	Asn	Ser	Phe	Ala	Ser	Ser	Leu	Trp
			260					265					270		
Leu	Met	Pro	Phe	Ser	Lys	Asn	Cys	Lys	Gly	Asp	Asn	Thr	Phe	Trp	Thr
		275					280					285			
His	Phe	Ser	Gly	Gly	Ala	Ala	Lys	Lys	Asp	Lys	Arg	Val	Tyr	His	Cys
	290					295					300				
Asp	Glu	Glu	Glu	Tyr	Gln	Ser	Lys	Tyr	Ser	Gly	Trp	Pro	Thr	Asn	Ile
305					310					315					320
Ile	Asn	Ile	Glu	Ile	Pro	Ser	Thr	Ser	Ala	Arg	Glu	Leu	Ala	Asp	Gly
				325					330					335	

Thr Leu Phe Lys Ala Ile Glu Asp Tyr Asp Pro Asp Ser Lys Arg Met
 340 345 350
 Leu His Gln Leu Lys Lys Tyr Val Pro Phe Phe Val Ile Arg Asn Ile
 355 360 365
 Ala His Arg Ser Ser Leu Ala Gly Phe Leu Leu Tyr His Asp Asp Pro
 370 375 380
 Val Phe Asn Pro Leu Thr Pro Trp Glu Arg Pro Pro Ile Lys Asn Val
 385 390 395 400
 Phe Cys Ile Tyr Gly Ala His Leu Lys Thr Glu Val Gly Tyr Tyr Phe
 405 410 415
 Ala Pro Ser Gly Lys Pro Tyr Pro Asp Asn Trp Ile Ile Thr Asp Ile
 420 425 430
 Ile Tyr Glu Thr Glu Gly Ser Leu Val Ser Arg Ser Gly Thr Val Val
 435 440 445
 Asp Gly Asn Ala Gly Pro Ile Thr Gly Asp Glu Thr Val Pro Tyr His
 450 455 460
 Ser Leu Ser Trp Cys Lys Asn Trp Leu Gly Pro Lys Val Asn Ile Thr
 465 470 475 480
 Met Ala Pro Gln Ile Leu Ile Gly Lys Ile Lys Gln Gln Pro Glu His
 485 490 495
 Asp Gly Ser Asp Val His Val Glu Leu Asn Val Asp His Glu His Gly
 500 505 510
 Ser Asp Ile Ile Ala Asn Met Thr Lys Ala Pro Arg Val Lys Tyr Ile
 515 520 525
 Thr Phe Tyr Glu Asp Ser Glu Ser Ile Pro Gly Lys Arg Thr Ala Val
 530 535 540
 Trp Glu Leu Asp Lys Ser Gly Tyr
 545 550

<210> 16

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 16

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190
 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205
 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350

Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly	355	360	365	
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	370	375	380	
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	385	390	395	400
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	405	410	415	
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	420	425	430	
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	435	440	445	
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met	450	455	460	
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln	465	470	475	480
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu	485	490	495	
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met	500	505	510	
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr	515	520	525	
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp	530	535	540	
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro	545	550	555	560
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser	565	570	575	
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly	580	585	590	
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp	595	600	605	
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser	610	615	620	
Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp	625	630	635	640
Leu	Val	Glu	Pro	Arg	Gln	Leu	Ser	Asn	Leu	Ser	Gln	Trp	Val	Ser	Gln	645	650	655	

Met Pro Phe Pro Met
660

<210> 17
<211> 387
<212> PRT
<213> Arabidopsis thaliana

<400> 17
Val Gly Ser Asn Val Tyr Pro Leu Ile Leu Val Pro Gly Asn Gly Gly
1 5 10 15
Asn Gln Leu Glu Val Arg Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val
20 25 30
Trp Cys Ser Ser Trp Leu Tyr Pro Ile His Lys Lys Ser Gly Gly Trp
35 40 45
Phe Arg Leu Trp Phe Asp Ala Ala Val Leu Leu Ser Pro Phe Thr Arg
50 55 60
Cys Phe Ser Asp Arg Met Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp
65 70 75 80
Tyr Gln Asn Ala Pro Gly Val Gln Thr Arg Val Pro His Phe Gly Ser
85 90 95
Thr Lys Ser Leu Leu Tyr Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser
100 105 110
Tyr Met Glu His Leu Val Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val
115 120 125
Asn Asp Gln Thr Ile Leu Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu
130 135 140
Ala Ala Ser Gly His Pro Ser Arg Val Ala Ser Gln Phe Leu Gln Asp
145 150 155 160
Leu Lys Gln Leu Val Glu Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro
165 170 175
Val Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu His Phe
180 185 190
Leu Asn Arg Thr Thr Pro Ser Trp Arg Arg Lys Tyr Ile Lys His Phe
195 200 205
Val Ala Leu Ala Ala Pro Trp Gly Gly Thr Ile Ser Gln Met Lys Thr
210 215 220
Phe Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asn Pro Leu Leu
225 230 235 240

Val Arg Arg His Gln Arg Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro
 245 250 255
 Ser Thr Lys Val Phe His Asp Arg Thr Lys Pro Leu Val Val Thr Pro
 260 265 270
 Gln Val Asn Tyr Thr Ala Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile
 275 280 285
 Gly Phe Ser Gln Gly Val Val Pro Tyr Lys Thr Arg Val Leu Pro Leu
 290 295 300
 Thr Glu Glu Leu Met Thr Pro Gly Val Pro Val Thr Cys Ile Tyr Gly
 305 310 315 320
 Arg Gly Val Asp Thr Pro Glu Val Leu Met Tyr Gly Lys Gly Gly Phe
 325 330 335
 Asp Lys Gln Pro Glu Ile Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn
 340 345 350
 Leu Ala Ser Leu Ala Ala Leu Lys Val Asp Ser Leu Asn Thr Val Glu
 355 360 365
 Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu
 370 375 380
 Lys Glu Ile
 385

<210> 18
 <211> 389
 <212> PRT
 <213> Arabidopsis thaliana

<400> 18
 Leu Lys Lys Glu Gly Leu Lys Ala Lys His Pro Val Val Phe Ile Pro
 1 5 10 15
 Gly Ile Val Thr Gly Gly Leu Glu Leu Trp Glu Gly Lys Gln Cys Ala
 20 25 30
 Asp Gly Leu Phe Arg Lys Arg Leu Trp Gly Gly Thr Phe Leu Cys Trp
 35 40 45
 Val Glu His Met Ser Leu Asp Asn Glu Thr Gly Leu Asp Pro Ala Gly
 50 55 60
 Ile Arg Val Arg Ala Val Ser Gly Leu Val Ala Ala Asp Tyr Phe Ala
 65 70 75 80
 Pro Gly Tyr Phe Val Trp Ala Val Leu Ile Ala Asn Leu Ala His Ile
 85 90 95
 Gly Tyr Glu Glu Lys Asn Met Tyr Met Ala Ala Tyr Asp Trp Arg Leu
 100 105 110

Ser Phe Gln Asn Thr Glu Arg Asp Gln Thr Leu Ser Arg Met Lys Ser
 115 120 125
 Asn Ile Glu Leu Met Val Ser Thr Asn Gly Gly Lys Lys Ala Val Ile
 130 135 140
 Val Pro His Ser Met Gly Val Leu Tyr Phe Leu His Phe Met Lys Trp
 145 150 155 160
 Val Glu Ala Pro Ala Pro Leu Gly Gly Gly Gly Gly Pro Asp Trp Cys
 165 170 175
 Ala Lys Tyr Ile Lys Ala Val Met Asn Ile Gly Gly Pro Phe Leu Gly
 180 185 190
 Val Pro Lys Ala Val Ala Gly Leu Phe Ser Ala Glu Ala Lys Asp Met
 195 200 205
 Arg Met Thr Arg Thr Trp Asp Ser Thr Met Ser Met Leu Pro Lys Gly
 210 215 220
 Gly Asp Thr Ile Trp Gly Gly Leu Asp Trp Ser Pro Glu Leu Pro Asn
 225 230 235 240
 Ala Pro Glu Met Glu Ile Tyr Ser Leu Tyr Gly Val Gly Ile Pro Thr
 245 250 255
 Glu Arg Ala Tyr Val Tyr Lys Leu Asn Gln Ser Pro Asp Ser Cys Ile
 260 265 270
 Pro Phe Gln Ile Phe Thr Ser Ala His Glu Glu Asp Glu Asp Ser Cys
 275 280 285
 Leu Lys Ala Gly Val Tyr Asn Val Asp Gly Asp Glu Thr Val Pro Val
 290 295 300
 Leu Ser Ala Gly Tyr Met Cys Ala Lys Ala Trp Arg Gly Lys Thr Arg
 305 310 315 320
 Phe Asn Pro Ser Gly Ile Lys Thr Tyr Ile Arg Glu Tyr Asn His Ser
 325 330 335
 Pro Pro Ala Asn Leu Leu Glu Gly Arg Gly Thr Gln Ser Gly Ala His
 340 345 350
 Val Asp Ile Met Gly Asn Phe Ala Leu Ile Glu Asp Ile Met Arg Val
 355 360 365
 Ala Ala Gly Gly Asn Gly Ser Asp Ile Gly His Asp Gln Val His Ser
 370 375 380
 Gly Ile Phe Glu Trp
 385

<210> 19
 <211> 1986
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1983)

<400> 19
 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg 240
 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt 288
 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt 336
 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt 384
 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac 432
 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt 480
 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta 528
 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att 576
 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile

180	185	190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp 195 200 205			624
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp 210 215 220			672
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn 225 230 235 240			720
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile 245 250 255			768
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile 260 265 270			816
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu 275 280 285			864
gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys 290 295 300			912
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu 305 310 315 320			960
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp 325 330 335			1008
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val 340 345 350			1056
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly 355 360 365			1104
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr 370 375 380			1152
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser 385 390 395 400			1200

aga	att	gag	aga	gta	aaa	atg	tta	caa	acg	tgg	ggg	ggg	ata	cca	tca	1248
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	
				405					410					415		
atg	cta	cca	aag	gga	gaa	gag	gtc	att	tgg	ggg	gat	atg	aag	tca	tct	1296
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	
			420					425					430			
tca	gag	gat	gca	ttg	aat	aac	aac	act	gac	aca	tac	ggc	aat	ttc	att	1344
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	
		435					440					445				
cga	ttt	gaa	agg	aat	acg	agc	gat	gct	ttc	aac	aaa	aat	ttg	aca	atg	1392
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met	
	450					455					460					
aaa	gac	gcc	att	aac	atg	aca	tta	tcg	ata	tca	cct	gaa	tgg	ctc	caa	1440
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln	
465					470					475					480	
aga	aga	gta	cat	gag	cag	tac	tcg	ttc	ggc	tat	tcc	aag	aat	gaa	gaa	1488
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu	
				485					490					495		
gag	tta	aga	aaa	aat	gag	cta	cac	cac	aag	cac	tgg	tcg	aat	cca	atg	1536
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met	
			500					505					510			
gaa	gta	cca	ctt	cca	gaa	gct	ccc	cac	atg	aaa	atc	tat	tgt	ata	tac	1584
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr	
		515					520					525				
ggg	gtg	aac	aac	cca	act	gaa	agg	gca	tat	gta	tat	aag	gaa	gag	gat	1632
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp	
	530					535					540					
gac	tcc	tct	gct	ctg	aat	ttg	acc	atc	gac	tac	gaa	agc	aag	caa	cct	1680
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro	
545					550					555					560	
gta	ttc	ctc	acc	gag	ggg	gac	gga	acc	gtt	ccg	ctc	gtg	gcg	cat	tca	1728
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser	
				565				570						575		
atg	tgt	cac	aaa	tgg	gcc	cag	ggg	gct	tca	ccg	tac	aac	cct	gcc	gga	1776
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly	
			580				585						590			
att	aac	gtt	act	att	gtg	gaa	atg	aaa	cac	cag	cca	gat	cga	ttt	gat	1824
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp	
		595					600					605				
ata	cgt	ggg	gga	gca	aaa	agc	gcc	gaa	cac	gta	gac	atc	ctc	ggc	agc	1872
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser	
	610					615					620					

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 20

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 20

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
 65 70 75 80

Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
 85 90 95

Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
 100 105 110

Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
 115 120 125

Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
 130 135 140

Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
 145 150 155 160

Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
 165 170 175

Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
 180 185 190

Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
 195 200 205

Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
 210 215 220
 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
 225 230 235 240
 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
 245 250 255
 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
 260 265 270
 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
 275 280 285
 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
 290 295 300
 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
 305 310 315 320
 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
 325 330 335
 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
 340 345 350
 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
 355 360 365
 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
 370 375 380
 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
 385 390 395 400
 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
 405 410 415
 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
 420 425 430
 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
 435 440 445
 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
 450 455 460
 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
 465 470 475 480
 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
 485 490 495
 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
 500 505 510

Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655
 Met Pro Phe Pro Met
 660

<210> 21
 <211> 1986
 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
 <221> CDS
 <222> (1)..(1983)

<400> 21
 atg ggc aca ctg ttt cga aga aat gtc cag aac caa aag agt gat tct 48
 Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15
 gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga 96
 Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30
 aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt 144
 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45
 att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg 192
 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
 50 55 60

aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg	240
Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
65 70 75 80	
att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288
Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
85 90 95	
ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336
Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	
100 105 110	
gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384
Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val	
115 120 125	
ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432
Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn	
130 135 140	
tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480
Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly	
145 150 155 160	
aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528
Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val	
165 170 175	
atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576
Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile	
180 185 190	
gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624
Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp	
195 200 205	
gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672
Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp	
210 215 220	
ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720
Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn	
225 230 235 240	
ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768
Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile	
245 250 255	
gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816
Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile	
260 265 270	
ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864
Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu	
275 280 285	

gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912
Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys	
290 295 300	
gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960
Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu	
305 310 315 320	
att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008
Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp	
325 330 335	
gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056
Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val	
340 345 350	
aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104
Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly	
355 360 365	
gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc	1152
Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr	
370 375 380	
att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca	1200
Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser	
385 390 395 400	
aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca	1248
Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser	
405 410 415	
atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct	1296
Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser	
420 425 430	
tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att	1344
Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile	
435 440 445	
cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg	1392
Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met	
450 455 460	
aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa	1440
Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln	
465 470 475 480	
aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa	1488
Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu	
485 490 495	
gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg	1536
Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met	
500 505 510	

gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
 515 520 525

ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
 530 535 540

gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
 545 550 555 560

gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
 565 570 575

atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
 580 585 590

att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
 595 600 605

ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
 610 615 620

gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920
 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
 625 630 635 640

ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag 1968
 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
 645 650 655

atg ccc ttc cca atg taa 1986
 Met Pro Phe Pro Met
 660

<210> 22

<211> 661

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 22

Met Gly Thr Leu Phe Arg Arg Asn Val Gln Asn Gln Lys Ser Asp Ser
 1 5 10 15

Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg
 20 25 30

Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
 35 40 45

Ile	Ser	Gly	Ser	Ala	Lys	Arg	Asn	Glu	Arg	Gly	Lys	Asp	Phe	Asp	Arg		
	50					55					60						
Lys	Arg	Asp	Gly	Asn	Gly	Arg	Lys	Arg	Trp	Arg	Asp	Ser	Arg	Arg	Leu		
	65				70				75						80		
Ile	Phe	Ile	Leu	Gly	Ala	Phe	Leu	Gly	Val	Leu	Leu	Pro	Phe	Ser	Phe		
				85					90					95			
Gly	Ala	Tyr	His	Val	His	Asn	Ser	Asp	Ser	Asp	Leu	Phe	Asp	Asn	Phe		
			100					105					110				
Val	Asn	Phe	Asp	Ser	Leu	Lys	Val	Tyr	Leu	Asp	Asp	Trp	Lys	Asp	Val		
		115					120					125					
Leu	Pro	Gln	Gly	Ile	Ser	Ser	Phe	Ile	Asp	Asp	Ile	Gln	Ala	Gly	Asn		
	130					135					140						
Tyr	Ser	Thr	Ser	Ser	Leu	Asp	Asp	Leu	Ser	Glu	Asn	Phe	Ala	Val	Gly		
	145				150					155					160		
Lys	Gln	Leu	Leu	Arg	Asp	Tyr	Asn	Ile	Glu	Ala	Lys	His	Pro	Val	Val		
				165				170						175			
Met	Val	Pro	Gly	Val	Ile	Ser	Thr	Gly	Ile	Glu	Ser	Trp	Gly	Val	Ile		
			180					185					190				
Gly	Asp	Asp	Glu	Cys	Asp	Ser	Ser	Ala	His	Phe	Arg	Lys	Arg	Leu	Trp		
		195					200					205					
Gly	Ser	Phe	Tyr	Met	Leu	Arg	Thr	Met	Val	Met	Asp	Lys	Val	Cys	Trp		
	210					215					220						
Leu	Lys	His	Val	Met	Leu	Asp	Pro	Glu	Thr	Gly	Leu	Asp	Pro	Pro	Asn		
	225				230					235					240		
Phe	Thr	Leu	Arg	Ala	Ala	Gln	Gly	Phe	Glu	Ser	Thr	Asp	Tyr	Phe	Ile		
				245					250					255			
Ala	Gly	Tyr	Trp	Ile	Trp	Asn	Lys	Val	Phe	Gln	Asn	Leu	Gly	Val	Ile		
			260					265					270				
Gly	Tyr	Glu	Pro	Asn	Lys	Met	Thr	Ser	Ala	Ala	Tyr	Asp	Trp	Arg	Leu		
	275						280					285					
Ala	Tyr	Leu	Asp	Leu	Glu	Arg	Arg	Asp	Arg	Tyr	Phe	Thr	Lys	Leu	Lys		
	290					295					300						
Glu	Gln	Ile	Glu	Leu	Phe	His	Gln	Leu	Ser	Gly	Glu	Lys	Val	Cys	Leu		
	305				310					315					320		
Ile	Gly	His	Ser	Met	Gly	Ser	Gln	Ile	Ile	Phe	Tyr	Phe	Met	Lys	Trp		
				325					330					335			
Val	Glu	Ala	Glu	Gly	Pro	Leu	Tyr	Gly	Asn	Gly	Gly	Arg	Gly	Trp	Val		
			340					345					350				

Asn	Glu	His	Ile	Asp	Ser	Phe	Ile	Asn	Ala	Ala	Gly	Thr	Leu	Leu	Gly	
		355					360					365				
Ala	Pro	Lys	Ala	Val	Pro	Ala	Leu	Ile	Ser	Gly	Glu	Met	Lys	Asp	Thr	
	370					375					380					
Ile	Gln	Leu	Asn	Thr	Leu	Ala	Met	Tyr	Gly	Leu	Glu	Lys	Phe	Phe	Ser	
385					390					395					400	
Arg	Ile	Glu	Arg	Val	Lys	Met	Leu	Gln	Thr	Trp	Gly	Gly	Ile	Pro	Ser	
				405					410					415		
Met	Leu	Pro	Lys	Gly	Glu	Glu	Val	Ile	Trp	Gly	Asp	Met	Lys	Ser	Ser	
			420					425					430			
Ser	Glu	Asp	Ala	Leu	Asn	Asn	Asn	Thr	Asp	Thr	Tyr	Gly	Asn	Phe	Ile	
		435					440					445				
Arg	Phe	Glu	Arg	Asn	Thr	Ser	Asp	Ala	Phe	Asn	Lys	Asn	Leu	Thr	Met	
	450					455					460					
Lys	Asp	Ala	Ile	Asn	Met	Thr	Leu	Ser	Ile	Ser	Pro	Glu	Trp	Leu	Gln	
465					470					475					480	
Arg	Arg	Val	His	Glu	Gln	Tyr	Ser	Phe	Gly	Tyr	Ser	Lys	Asn	Glu	Glu	
				485					490					495		
Glu	Leu	Arg	Lys	Asn	Glu	Leu	His	His	Lys	His	Trp	Ser	Asn	Pro	Met	
			500					505					510			
Glu	Val	Pro	Leu	Pro	Glu	Ala	Pro	His	Met	Lys	Ile	Tyr	Cys	Ile	Tyr	
		515					520					525				
Gly	Val	Asn	Asn	Pro	Thr	Glu	Arg	Ala	Tyr	Val	Tyr	Lys	Glu	Glu	Asp	
	530					535					540					
Asp	Ser	Ser	Ala	Leu	Asn	Leu	Thr	Ile	Asp	Tyr	Glu	Ser	Lys	Gln	Pro	
545					550					555					560	
Val	Phe	Leu	Thr	Glu	Gly	Asp	Gly	Thr	Val	Pro	Leu	Val	Ala	His	Ser	
				565					570					575		
Met	Cys	His	Lys	Trp	Ala	Gln	Gly	Ala	Ser	Pro	Tyr	Asn	Pro	Ala	Gly	
			580					585					590			
Ile	Asn	Val	Thr	Ile	Val	Glu	Met	Lys	His	Gln	Pro	Asp	Arg	Phe	Asp	
		595					600					605				
Ile	Arg	Gly	Gly	Ala	Lys	Ser	Ala	Glu	His	Val	Asp	Ile	Leu	Gly	Ser	
	610					615					620					
Ala	Glu	Leu	Asn	Asp	Tyr	Ile	Leu	Lys	Ile	Ala	Ser	Gly	Asn	Gly	Asp	
625					630					635					640	
Leu	Val	Glu	Pro	Arg	Gln	Leu	Ser	Asn	Leu	Ser	Gln	Trp	Val	Ser	Gln	
				645					650					655		

Met Pro Phe Pro Met
660

<210> 23
<211> 2312
<212> genomic DNA
<213> Schizosaccharomyces pombe

<400> 23
atggcgtctt ccaagaagag caaaactcat aagaaaaaga aagaagtcaa atctcctatc 60
gacttaccaa attcaaagaa accaactcgc gctttgagtg agcaaccttc agcgtccgaa 120
acacaatctg tttcaaataa atcaagaaaa tctaaatttg gaaaaagatt gaattttata 180
ttgggcgcta ttttgggaat atgcggtgct ttttttttcg ctggttgaga cgacaatgct 240
gttttcgacc ctgctacgtt agataaattt gggaatatgc taggctcttc agacttgttt 300
gatgacatta aaggatattt atcttataat gtgtttaagg atgcacctt tactacggac 360
aagccttcgc agtctcctag cggaaatgaa gttcaagttg gtcttgatat gtacaatgag 420
ggatatcgaa gtgaccatcc tgttattatg gttcctggtg ttatcagctc aggattagaa 480
agttggtcgt ttaataattg ctcgattcct tacttttagga aacgtctttg gggtagctgg 540
tctatgctga aggcaatgtt ccttgacaag caatgctggc ttgaacattt aatgcttgat 600
aaaaaaaccg gcttggatcc gaaggggaatt aagctgctgag cagctcaggg gtttgaagca 660
gctgattttt ttatcacggg ctattggatt tggagtaaaag taattgaaaa ccttgctgca 720
attggttatg agcctaataa catgttaagt gcttcttacg attggcgggt atcatatgca 780
aatttagagg aacgtgataa atatttttca aagttaaaaa tgttcattga gtacagcaac 840
attgtacata agaaaaaggt agtgttgatt tctactcca tgggttcaca ggttacgtac 900
tattttttta agtgggttga agctgagggc tacggaaatg gtggaccgac ttgggttaat 960
gatcatattg aagcatttat aaatgtgagt ctcgatggtt gtttgactac gtttctaact 1020
tttgaataga tatcgggatc tttgattgga gcacccaaaa cagtggcagc gcttttatcg 1080
ggtgaaatga aagatacagg tattgtaatt acattaaaca tgtaaatatt taatttttgc 1140
taaccgtttt aagctcaatt gaatcagttt tcggtctatg ggtaagcaat aaattgttga 1200
gatttgttac taatttactg tttagtttgg aaaaattttt ttcccgttct gaggtatatt 1260
caaaaataca aatgtgctct acttttttcta acttttaata gagagccatg atggttcgca 1320
ctatgggagg agttagttct atgcttccta aaggaggcga tgttgatatg ggaaatgcca 1380
gttgggtaag aaatatgtgc tgtaattttt ttattaatat ttaggctcca gatgatctta 1440
atcaaacaaa tttttccaat ggtgcaatta ttcgatatag agaagacatt gataaggacc 1500
acgatgaatt tgacatagat gatgcattac aattttttaa aaatgttaca gatgacgatt 1560
ttaaagtcac gctagcgaaa aattattccc acggtcttgc ttggactgaa aaagaagtgt 1620
taaaaaataa cgaaatgccg tctaaatgga taaatccgct agaagtaaga acattaaagt 1680
tactaaatta tactaaccga aatagactag tcttccttat gctcctgata tgaatttta 1740
ttgcgttcac ggggtcggaa aaccaactga gagaggttat tattatacta ataactctga 1800
ggggcaacct gtcattgatt cctcgggtta tgatggaaca aaagttgaaa atgtgagaga 1860
atztatgttt caaacattct attaaactgt ttattagggg attggttatg atgatggtga 1920
tggaacttta ccaatattag cccttggttt ggtgtgcaat aaagtttggc aaacaaaaag 1980
gtttaatcct gctaatacaa gtatcacaaa ttatgaaatc aagcatgaac ctgctgcgtt 2040
tgatctgaga ggaggacctc gctcggcaga acacgtcgat atacttggac attcagagct 2100
aaatgtatgt tcattttacc ttacaaattt ctattactaa ctcttgaaat aaggaaatta 2160
ttttaaaagt ttcacagggc catggtgact cggtagcaaa ccgttatata tcagatatcc 2220
agtacggaca taagttttgt agattgcaat taactaacta accgaacagg gaaataataa 2280
atgagataaa tctcgataaa cctagaaatt aa 2312

<210> 24
<211> 3685
<212> genomicDNA
<213> Arabidopsis thaliana

<400> 24

atgcccctta	ttcatcggaa	aaagccgacg	gagaaacccat	cgacgccgcc	atctgaagag	60
gtggtgcacg	atgaggattc	gcaaaagaaa	ccacacgaat	cttccaaatc	ccaccataag	120
aaatcgaacg	gaggagggaa	gtggtcgtgc	atcgattcctt	gttggttggtt	cattgggtgt	180
gtgtgtgtaa	cctggtgggtt	tcttctcttc	ctttacaacg	caatgcctgc	gagcttccct	240
cagtatgtaa	cggagcgaat	cacgggtcct	ttgcctgacc	cgcccgggtgt	taagctcaaa	300
aaagaaggtc	ttaaggcgaa	acatcctgtt	gtcttcattc	ctgggattgt	caccgggtggg	360
ctcgagcttt	gggaaggcaa	acaatgcgct	gatggtttat	ttagaaaacg	tttgtggggt	420
ggaacttttg	gtgaagtcta	caaaagggtga	gctcaacaat	tctcactctt	cctttatatt	480
gggattttgga	ttggatctga	tgagatcacg	cacttggtgc	ttcttcaaca	tactcaaac	540
tttaattcca	tgtttgtctg	tcttactctt	tacttttttt	tttttttgat	gtgaaacgct	600
attttcttaa	gagactattt	ctgtatgtgt	aaggtaagcg	ttccaaggac	gtaattggct	660
tggactattt	ctgtttgatt	gttaacttta	ggatataaaa	tagctgcctt	ggaatttcaa	720
gtcatcttat	tgccaaatct	gttgctagac	atgccctaga	gtccgttcat	aacaagttac	780
ttcctttact	gtcgttgctg	gtagatttag	ctttgtgtag	cgtataatga	agtagtggtt	840
tatgttttgt	tgggaataga	gaagttctaa	ctacatctgt	ggaaagtgtg	ttcaggctgt	900
gatagaggac	tgttgcttta	ttattcaact	atgtatatgt	gtaattaaag	ctagttcctt	960
tttgatcttt	cagctcaatg	tgcttttctc	aatttttttc	tcaatttcaa	agtttcacat	1020
cgagtttatt	cacatgtctt	gaatttcgtc	catcctcggt	ctgttatcca	gctttgaact	1080
cctcccgcac	ctgctatgga	tatattaaaa	aaaaagtgtt	ttgtgggttg	catctttggt	1140
acgatctgca	tcttcttctt	tcggctcagt	gttcatgttt	ttgctatggg	agagatgggc	1200
aatgttattg	ttgatggtaa	cagtgtgata	gttgatagta	tcttaactaa	tcaattatct	1260
ctttgattca	ggcctctatg	ttgggtggaa	cacatgtcac	ttgacaatga	aactgggttg	1320
gatccagctg	gtattagagt	tcgagctgta	tcaggactcg	tggctgctga	ctactttgct	1380
cctggctact	ttgtctgggc	agtgtgatt	gctaaccctg	cacatattgg	atatgaagag	1440
aaaaatatgt	acatggctgc	atatgactgg	cggttttcgt	ttcagaacac	agaggttcct	1500
ttctcatcgt	tctttctatt	attctgttcc	atgttacgtt	tctttcttca	ttacttaagg	1560
cttaaataatg	tttcatgttg	aattaatagg	tacgtgatca	gactcttagc	cgtatgaaaa	1620
gtaatataga	gttgatggtt	tctaccaacg	gtggaaaaaa	agcagttata	gttccgcatt	1680
ccatgggggt	cttgatattt	ctacatttta	tgaagtgggt	tgaggcacca	gctcctctgg	1740
gtggcggggg	tgggccaagt	tgggtgtgca	agtatatata	ggcgggtgat	aacattgggt	1800
gaccatttct	tgggttcca	aaagctgttg	cagggttttt	ctctgctgaa	gcaaaaggatg	1860
ttgcagttgc	caggtattga	atatctgctt	atacttttga	tgatcagaac	cttggctctg	1920
gaactcaaag	ttattctact	aaatatcaat	tctaataaca	ttgctatatt	atcgctgcaa	1980
ctgacattgg	ttgattattt	ttgctgctta	tgtaaactgaa	actctcttga	gattagacaa	2040
atgatgaatt	gataattctt	acgcattgct	ctgtgatgac	cagtttctta	gcttcgacga	2100
taacatttgt	catactgtct	tttggagggc	attgaatttt	gctatggaaa	gcgctggagc	2160
ttccatgctt	gcattcttta	ccaattagcg	ttattctgct	tctttcaatt	ttcttgtata	2220
tgcatctatg	gtcttttatt	tcttcttaat	taaagactcg	ttggattagt	tgctctatta	2280
gtcacttggt	tccttaatat	agaactttac	tttcttcgaa	aattgcagag	cgattgcccc	2340
aggattctta	gacaccgata	tatttagact	tcagaccttg	cagcatgtaa	tgagaatgac	2400
acgcacatgg	gactcaacaa	tgtctatggt	accgaaggga	ggtgacacga	tatggggcgg	2460
gcttgattgg	tcaccggaga	aaggccacac	ctgttggtggg	aaaaagcaaa	agaacaacga	2520
aacttggtgt	gaagcagggtg	aaaacggagt	ttccaagaaa	agtcctgtta	actatggaag	2580
gatgatatct	tttgggaaag	aagtagcaga	ggctgcgcca	tctgagatta	ataatattga	2640
ttttcgagta	aggacatata	aatcataata	aaccttgtag	atthttgtgat	tgtatgatga	2700
atatctgtac	atthttatctg	gtgaagggtg	ctgtcaaagg	tcagagtatc	ccaaatcaca	2760
cctgtcgtga	cgtgtggaca	gagtaccatg	acatgggaat	tgctgggatc	aaagctatcg	2820
ctgagtataa	ggtctacact	gctgggtgaag	ctatagatct	actacattat	gttgctccta	2880
agatgatagg	gcgtgtgcc	gctcatttct	cttatggaat	tgctgatgat	ttggatgaca	2940
ccaagtatca	agatcccaaa	tactggtcaa	atccgttaga	gacaaaagtaa	gtgatttctt	3000
gattccaact	gtatccttcg	tctgtatgca	ttatcagtct	ttttgttttc	ggtcttggtg	3060
gatatggttt	tcagctcaaa	gcttacaagg	ctgtttctga	gcctttctca	aaaaggcttg	3120
ctcagtaata	ttgaggtgct	aaagttgata	catgtgactc	ttgcttataa	atcctccgtt	3180
tggtttggtc	tgctttttca	gattaccgaa	tgctcctgag	atggaaatct	actcattata	3240
cggagtgggg	ataccaacgg	aacgagcata	cgtatacaag	cttaaccagt	ctcccgcacg	3300
ttgcatcccc	tttcagatat	tcacttctgc	tcacgaggag	gacgaagata	gctgtctgaa	3360
agcaggaggt	tacaatgtgg	atggggatga	aacagtaccc	gtcctaagtg	ccgggtacat	3420

```

gtgtgcaaaa gctgtggcgtg gcaagacaag attcaaccct tccggaatca agacttatat 3480
aagagaatac aatcactctc cgccggctaa cctgttggaa gggcgcgggg cgagagtggt 3540
tgcccatgtt gatcatcatg gaaactttgc tttgatcgaa gatcatcatga gggttgccgc 3600
cggaggtaac gggcttgata taggacatga ccaggtccac tctggcatat ttgaatggtc 3660
ggagcgtatt gacctgaagc tgtga                                     3685

```

<210> 25

<211> 402

<212> cDNA

<213> *Arabidopsis thaliana*

<220>

<221> CDS

<222> (120) .. (401)

<400> 25

```

agaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60

```

```

ctggacgaga ttgacaaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagat 119

```

```

atg ccc ctt att cat cgg aaa aag ccg acg gag aaa cca tcg acg ccg 167
Met Pro Leu Ile His Arg Lys Lys Pro Thr Glu Lys Pro Ser Thr Pro
  1             5             10             15

```

```

cca tct gaa gag gtg gtg cac gat gag gat tcg caa aag aaa cca cac 215
Pro Ser Glu Glu Val Val His Asp Glu Asp Ser Gln Lys Lys Pro His
      20             25             30

```

```

gaa tct tcc aaa tcc cac cat aag naa tcg aac gga gga ggg aag tgg 263
Glu Ser Ser Lys Ser His His Lys Xaa Ser Asn Gly Gly Gly Lys Trp
      35             40             45

```

```

tcg tgc atc gat tct tgt tgt tgg ttc att ggg tgt gtg tgt gta acc 311
Ser Cys Ile Asp Ser Cys Cys Trp Phe Ile Gly Cys Val Cys Val Thr
      50             55             60

```

```

tgg tgg ttt ctt ctc ttc ctt tac aac gca atg cct gcg agc ttc cct 359
Trp Trp Phe Leu Leu Phe Leu Tyr Asn Ala Met Pro Ala Ser Phe Pro
      65             70             75             80

```

```

cag tat gta acg gag ccg aat cac gng tcc ttt gcc tta ccc g 402
Gln Tyr Val Thr Glu Pro Asn His Xaa Ser Phe Ala Leu Pro
      85             90

```

<210> 26

<211> 643

<212> cDNA

<213> *Zea mays*

<220>

<221> CDS

<222> (1) .. (402)

<400> 26

```

cgg gag aaa ata gct gct ttg aag ggg ggt gtt tac tta gcc gat ggt 48
Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
  1              5              10              15

gat gaa act gtt cca gtt ctt agt gcg ggc tac atg tgt gcg aaa gga 96
Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
              20              25              30

tgg cgt ggc aaa act cgt ttc agc cct gcc ggc agc aag act tac gtg 144
Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
              35              40              45

aga gaa tac agc cat tcg cca ccc tct act ctc ctg gaa ggc agg ggc 192
Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
  50              55              60

acc cag agc ggt gca cat gtt gat ata atg ggg aac ttt gct cta att 240
Thr Gln Ser Gly Ala His Val Asp Ile Met Gly Asn Phe Ala Leu Ile
  65              70              75              80

gag gac gtc atc aga ata gct gct ggg gca acc ggt gag gaa att ggt 288
Glu Asp Val Ile Arg Ile Ala Ala Gly Ala Thr Gly Glu Glu Ile Gly
              85              90              95

ggc gat cag gtt tat tca gat ata ttc aag tgg tca gag aaa atc aaa 336
Gly Asp Gln Val Tyr Ser Asp Ile Phe Lys Trp Ser Glu Lys Ile Lys
              100              105              110

ttg aaa ttg taa cct atg gga agt taa aga agt gcc gac ccg ttt att 384
Leu Lys Leu
              115

gcg ttc caa agt gtc ctg cctgagtgca actctggatt ttgcttaaatt 432

attgtaatttt ttcacgcttc attcgtccct ttgtcaaatt tacatttgac aggacgccaa 492

tgcgatacga tgttgtagcg ctattttcag cattgtatat taaactgtac aggtgtaagt 552

tgcatattgcc agctgaaatt gtgtagtcgt tttctttacg atttaaatanc aagtggcgga 612

gcagtgcccc aagcnaaaaa aaaaaaaaaa a 643

```

<210> 27

<211> 115

<212> PRT

<213> Zea mays

<400> 30

```

Arg Glu Lys Ile Ala Ala Leu Lys Gly Gly Val Tyr Leu Ala Asp Gly
  1              5              10              15
Asp Glu Thr Val Pro Val Leu Ser Ala Gly Tyr Met Cys Ala Lys Gly
              20              25              30
Trp Arg Gly Lys Thr Arg Phe Ser Pro Ala Gly Ser Lys Thr Tyr Val
              35              40              45
Arg Glu Tyr Ser His Ser Pro Pro Ser Thr Leu Leu Glu Gly Arg Gly
  50              55              60

```

Thr	Gln	Ser	Gly	Ala	His	Val	Asp	Ile	Met	Gly	Asn	Phe	Ala	Leu	Ile
65					70					75					80
Glu	Asp	Val	Ile	Arg	Ile	Ala	Ala	Gly	Ala	Thr	Gly	Glu	Glu	Ile	Gly
			85					90						95	
Gly	Asp	Gln	Val	Tyr	Ser	Asp	Ile	Phe	Lys	Trp	Ser	Glu	Lys	Ile	Lys
			100					105					110		
Leu	Lys	Leu													
		115													

<210> 28
 <211> 516
 <212> cDNA
 <213> *Neurospora crassa*

<400> 28
 ggtggcggaag acganggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
 accctctaga gacacgacta ccnttgcacc cagcctcaag gtntacngtt tntatgggta 120
 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcata 180
 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggg gtgattttgg 240
 gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
 aatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
 cagaacggtt caatccgaga ggagggccga atacggcgga cttaaataatg tagaaaaggt 420
 tgaaatttat gaagagtaat taaatacggc acataggtta ctcaatagta tgactaatta 480
 aaaaaaatt ttttttctaa aaaaaaaaaa aaaaaa 516

<210> 29
 <211> 1562
 <212> genomic DNA
 <213> *Arabidopsis thaliana*

<400> 29
 atgaaaaaaaa tatcttcaca ttattcggta gtcatagcga tactcgttgt ggtgacgatg 60
 acctcgatgt gtcaagctgt gggtagcaac gtgtaccctt tgattcttgt tccaggaaac 120
 ggaggttaacc agctagaggt acggctggac agagaataca agccaagtag tgtctgggtg 180
 agcagctggt tatatccgat tcataagaag agtgggtgat ggtttaggct atggttcgat 240
 gcagcagtggt tattgtctcc ctccaccagg tgcttcagcg atcgaatgat gttgtactat 300
 gaccctgatt tggatgatta ccaaaatgct cctgggtgtcc aaaccgggt tcctcatttc 360
 ggttcgacca aatcacttct atacctcgac cctcgtctcc ggtagtagtact ttccaagata 420
 tatcattttg ggacatttgc ataatagaac aaatagacat aaatttgggg gattatttgt 480
 atatcaatat ccattttatat gctagtcggg aatgtgagtg ttatgttagt atagttaatg 540
 tgagtgttat gtgattttcc attttaaatg aagctagaaa gttgtcgttt aataatgttg 600
 ctatgtcatg agaattataa ggacactatg taaatgtagc ttaataataa ggtttgattt 660
 gcagagatgc cacatcttac atggaacatt tgggtgaaagc tctagagaaa aaatgcgggt 720
 atgttaacga ccaaaccatc ctaggagctc catatgattt caggtagcgc ctggctgctt 780
 cgggccaccc gtcccgtgta gcctcacagt tcctacaaga cctcaaacia ttggtggaaa 840
 aaactagcag cgagaacgaa ggaaagccag tgatactcct ctcccatagc ctaggaggac 900
 ttttcgtcct ccatttcctc aaccgtacca ccccttcgat gcgccgcaag tacatcaaac 960
 actttgttgc actcgtgctg ccattgggtg ggacgatctc tcagatgaag acatttgctt 1020
 ctggcaacac actcgtgtgc ctttagtcta accctttgct ggtcagacgg catcagagga 1080
 cctccgagag taaccaatgg ctacttccat ctaccaaagt gtttcacgac agaactaaac 1140
 cgcttgctgt aactccccag gttaactaca cagcttacga gatggatcgg ttttttgag 1200
 acattggatt ctcaacaagg gttgtgcctt acaagacaag agtgttcctt ttaacagagg 1260
 agctgatgac tccgggagtg ccagtcactt gcatatatgg gagaggagtt gataaccgg 1320
 aggttttgat gtatggaaaa ggaggattcg ataagcaacc agagattaag tatggagatg 1380
 gagatgggac ggttaatttg gcgagcttag cagctttgaa agtcgatagc ttgaacaccg 1440

```

tagagattga tggagtttcg catacatcta tacttaaaga cgagatcgca cttaaagaga 1500
ttatgaagca gatttcaatt attaattatg aattagccaa tgtaaatgcc gtcaatgaat 1560
ga 1562

```

<210> 30

<211> 3896

<212> genomic DNA

<213> Arabidopsis thaliana

<400> 30

```

atgggagcga attcgaaatc agtaacggct tccttcaccg tcatcgccgt ttttttcttg 60
atgtgcggtg gccgaactgc ggtggaggat gagaccgagt ttcacggcga ctactcgaag 120
ctatcgggta taatcattcc gggatttgcg tcgacgcagc tacgagcgtg gtcgatcctt 180
gactgtccat aactccggtt ggacttcaat ccgctcgacc tcgtatggct agacaccact 240
aagggtccgtg atcttcattt ccttcgctcc ttattctgtc ggtcgagtc cttgttgatg 300
aattccaagc gaaatatagc aatgaagcat gtctcgctc tcttattgat tcgttcatta 360
gtcaacagtg acgcttctga atctgagttt agagtcatat aaaacagctg actcggcgag 420
tgtttcccat cgcttttggg tcgctaaatg tagcgcaatg aatgtgtaat tagtctgcgc 480
tttttattca actagatctg caagtttttc agagtgtcga atagtagtta gaaaatgtta 540
ggtcatttta cttgtgcatt gtgattcttt tgggtgttgc ttactgatcg acgtgatgga 600
tggtttacag cttctttctg ctgtcaactg ctggtttaag tgtatgggtc tagatcctta 660
taatcaaaca gaccatcccg agtghtaagtc acggcctgac agtggctctt cagccatcac 720
agaattggat ccagggttaca taacaggtag ttccggattt ttctttcttt tgagtcttct 780
tcaatttgat atcatcttgt tgtgatataa tatggctaag ttcattaatt tggccaattt 840
tcaggtcttc tttctactgt ctggaaagag tggcttaagt ggtgtgttga gtttgggtata 900
gaagcaaagc caattgtcgc tgttccatac gattggagat tgtcaccaac caaattggaa 960
gagcgtgacc tttactttca caagctcaag ttagtcctta tcaggctaag gtcttttctt 1020
ttctcttttt atgtaagata agctaagagc tctggtcgtc ttcttttttg caggttgacc 1080
tttgaagctg ctttaaaact ccgtggcgcc ccttctatag tatttgccca ttcaattgggt 1140
aataatgtct tcagatactt tctggaatgg ctgaggctag aaattgcacc aaaacattat 1200
ttgaagtggc ttgatcagca tatccatgct tatttcgctg ttggtaccgg cctactatcc 1260
ttaagttacc attttatttt ttctctaatt gggggagtta tgttgtgact tactggattg 1320
agctcgatac ctgatttggt gttgatttag gagctcctct tcttggttct gttgaggcaa 1380
tcaaactctc tctctctggt gtaacgtttg gccttctgt ttctgagggt acctctgact 1440
tctctttagt ttttaagtag tgatatcaac caggctttat aactcactgg attttccttt 1500
tgaaagtatt acttttggtt attgaactgc tgtacgcgat atggtatctg tagatcttga 1560
agtgtagtt atcaaagaac atattgtggg tagtatacct gtcagcggcc ttagctaata 1620
caaccaaac acatgtacac tgatttagtt ttcagattat tatggtagac ttttaagttga 1680
gaagaaactt tgactgaaat ctttttattt taataggcta tgatttgttt attgaaatca 1740
tgtgacatat tgacatgcgc ttctcatggt tttgtttggc aaggcttcag ggaactgctc 1800
ggttggtgtc caattctttt gcgtcgtcat tgtggcttat gccattttca aagaattgca 1860
aggggtgata cacattctgg acgcattttt ctgggggtgc tgcaaaagaa gataagcgcg 1920
tataccactg tgatgaagag gaatatcaat caaaatattc tggctggccg acaaataata 1980
ttaacattga aattccttcc actagcgggt agactctgta tatgcaactg taacactaac 2040
aaaagtttca ccaagaatgt tcaactctcat atttcgttcc tttgatgtgt atccatcagt 2100
tacagaaaca gctctagtca acatgaccag catggaatgt ggccttccca ccctttgtc 2160
tttcacagcc cgtgaactag cagatgggac tcttttcaaa gcaatagaag actatgaccc 2220
agatagcaag aggatgttac accagttaaa gaagtacgta cttttctttg tgataagaaa 2280
tattgctcat cgatcatcac ttgctggctt cttgtacgtc aaattgtttt gtttaaatct 2340
ctatatcaat tgttcatatg ctttgtcttt cttactataa gaaacaagta taatcagaaa 2400
ccttattatt gattatcagt tctctcctta tattatggaa tgtctttttc gtttacagtt 2460
atgaatgcaa aagggggtat tttagttgat tgattctctc attctctagt ttgttttgac 2520
taatagcgtc aattttgttt ttctagcaaa tctttgtgaa ttatatataa catgctaact 2580
atacttttca gggtgtatca tgatgaccct gtttttaatc ctctgactcc ttggggagaga 2640
ccacctataa aaaatgtatt ttgcatatat ggtgctcatc taaagacaga ggtatgatgc 2700
attctcaata tcacattatg cgttgacttt gttattatat tccccatttg gtttgcaata 2760

```

```

tctttttgaa ttatgattta tcttctccct tgcattcttat gctattaagc gttaaaggta 2820
ctaaatgtat gaagctgtct gtcataagggtt gggtattact ttgccccaaag tggcaaacct 2880
tatcctgata attggatcat cacggatatac atttatgaaa ctgaagggttc cctcgtgtca 2940
aggtaatttt ccgcaatggc agaagtaaaa caggaaggca aagtcttctg tatcagtcta 3000
gtggcatgtt atctcagttg cataagcaaa ttattaaaca actaaaattt aagtactttt 3060
ttatcattcc ttttgagctt agtggatgat cagtggctta aagtgggaag aggtgttgca 3120
tgaacatga cacttgatc aaagataact agcaaaaaca aactaaccca tttctgaatt 3180
tcatattatt aggagtagtc gtgcttttaa aaaatttggt ttaagaaacc gaaaaactag 3240
ttcatatctt gattgtgcaa tatctgcagg tctggaactg tggttgatgg gaacgctgga 3300
cctataactg gggatgagac ggtaagctca gaagttgggt ttgaaattat cttcttgcaa 3360
actactgaag actaagataa tacttgcttc tggaaactg cttgctatgt tctctagtac 3420
actgcaatat tgactctccg ctacttttat tgattatgaa attgatctct tatagtacc 3480
ctatcattca ctctcttggt gcaagaattg gctcggacct aaagttaaca taacaatggc 3540
tccccaggtt ctctttttta gttcctcacc ttatatagat caaactttaa gtgtactttt 3600
ctggttatgt gttgatttac ctccaatttg ttctttctaa aaatcatata tctctgtact 3660
cctcaagaac ttgtattaat ctaaacgaga ttctcattgg gaaaataaaa caacagccag 3720
aacacgatgg aagcgacgta catgtggaac taaatgttga tcatgagcat gggcagaca 3780
tcatagctaa catgacaaaa gcaccaaggg ttaagtacat aaccttttat gaagactctg 3840
agagcattcc ggggaagaga accgcagtct gggagcttga taaaagtggg tattaa 3896

```

<210> 31
 <211> 709
 <212> cDNA
 <213> tomato

```

<400> 31
ctggggccaa aagtgaacat aacaaggaca ccacagtcag agcatgatgt tcagatgtac 60
aagtgcattc aaatatagag catcaacatg gtgaagatat cattcccaat atgacaaagt 120
tacctacaat gaagtacata acctattatg aggattctga aagttttcca gggacaagaa 180
cagcagtttg ggagcttgat aaagcaaatc acaggaacat tgtcagatct ccagctttga 240
tgcgggagct gtggcttgag atgtggcatg atattcatcc tgataaaaag tccaagtttg 300
ttacaaaagg tgggtgtctga tcctcactat tttcttctat aaatgtttga gtttgtattg 360
acattgtaag tattgcaaca aaaagcaaag cgtgggcctc tgagggatga ggactgctat 420
tggtgattac ggaaagctcg atgtgcatgg gctgaacatt gtgaatacag gttagaatat 480
tcaaattata ttttgcaaaa tattctcttt ttgtgtattt aggccacctt tccccgggtca 540
caacgatgca gatatgtatt cggggatggt cacctgggac agagttgcag attgaagagt 600
tctacatctc acatcctgtc acactatgtg tgatatttaa gaaactttgt ttggcggaac 660
aacaagtttg cacaacatt tgaagaagaa agcgaaatga ttcagagag 709

```

<210> 32
 <211> 7
 <212> PRT
 <213> Conserved Sequence

<400> 7
 Phe Xaa Lys Trp Val Glu Ala
 1 5